

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/612,914A

DATE: 09/04/2001
TIME: 12:34:34

Input Set : N:\Crif3\RULE60\09612914A.txt
Output Set: N:\CRF3\09042001\I612914A.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Hanna, Nabil

7 Newman, Roland A.

8 Reff, Mitchell E.

10 (ii) TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
11 Therapy

13 (iii) NUMBER OF SEQUENCES: 59

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

17 (B) STREET: 699 Prince Street

18 (C) CITY: Alexandria

19 (D) STATE: VA

20 (E) COUNTRY: USA

21 (F) ZIP: 22314-3187

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/612,914A

C--> 31 (B) FILING DATE: 10-Jul-2000

37 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US 08/523,894

36 (B) FILING DATE: 06-SEP-1995

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Teskin, Robin L.

41 (B) REGISTRATION NUMBER: 35,030

42 (C) REFERENCE/DOCKET NUMBER: 012712-165

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: 703-836-6620

46 (B) TELEFAX: 703-836-2021

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 420 base pairs

53 (B) TYPE: nucleic acid

54 (C) STRANDEDNESS: single

55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: DNA (genomic)

59 (vi) ORIGINAL SOURCE:

60 (A) ORGANISM: Monkey

62 (viii) POSITION IN GENOME:

63 (A) CHROMOSOME/SEGMENT: light variable domain of CE9.1

65 (ix) FEATURE:

66 (A) NAME/KEY: CDS

Duplicate
ENTERED

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67          (B) LOCATION: 4..420
69      (ix) FEATURE:
70          (A) NAME/KEY: mat_peptide
71          (B) LOCATION: 61..420
74      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
76 GAC ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA      48
77 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg
78 -19 -15 -10 -5
80 TGG GTC TTG TCC CAG GTG CAG CTG CAG GAG GCG GGC CCA GGA CTG GTG      96
81 Trp Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Gly Leu Val
82 1 5 10
84 AAG CCT TCG GAG ACC CTG TCC CTC ACC TGC AGT GTC TCT GGT GGC TCC      144
85 Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser
86 15 20 25
88 ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA GGG AAG      192
89 Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys
90 30 35 40
92 GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT      240
93 Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn
94 45 50 55 60
96 TAC AAT CCC TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC      288
97 Tyr Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser
98 65 70 75
100 AAG AAC CTC TTC TCC CTG AAA CTG AGG TCT GTG ACC GCC GCG GAC ACG      336
101 Lys Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr
102 80 85 90
104 GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT CAC TGG TTA      384
105 Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu
106 95 100 105
108 TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC      420
109 Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser
110 110 115 120
113 (2) INFORMATION FOR SEQ ID NO: 2:
115      (i) SEQUENCE CHARACTERISTICS:
116          (A) LENGTH: 139 amino acids
117          (B) TYPE: amino acid
118          (D) TOPOLOGY: linear
120      (ii) MOLECULE TYPE: protein
122      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
124 Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp
125 -19 -15 -10 -5
127 Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Gly Leu Val Lys
128 1 5 10
130 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile
131 15 20 25
133 Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly
134 30 35 40 45
136 Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr
137 50 55 60

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139 Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys
140          65          70          75
142 Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala
143          80          85          90
145 Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu
146          95          100          105
148 Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser
149 110          115          120
151 (2) INFORMATION FOR SEQ ID NO: 3:
153     (i) SEQUENCE CHARACTERISTICS:
154         (A) LENGTH: 387 base pairs
155         (B) TYPE: nucleic acid
156         (C) STRANDEDNESS: single
157         (D) TOPOLOGY: linear
159     (ii) MOLECULE TYPE: DNA (genomic)
161     (vi) ORIGINAL SOURCE:
162         (A) ORGANISM: Monkey
164     (viii) POSITION IN GENOME:
165         (A) CHROMOSOME/SEGMENT: heavy variable domain of CE9.1
167     (ix) FEATURE:
168         (A) NAME/KEY: CDS
169         (B) LOCATION: 4..387
171     (ix) FEATURE:
172         (A) NAME/KEY: mat_peptide
173         (B) LOCATION: 61..387
176     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
178 ACC ATG GCC TGG GCT CTG CTG CTC CTC GGC CTC CTT GCT CAC TTT ACA      48
179 Met Ala Trp Ala Leu Leu Leu Gly Leu Leu Ala His Phe Thr
180 -19          -15          -10          -5
182 GAC TCT GCG GCC TCC TAT GAG TTG AGT CAG CCT CGC TCA GTG TCC GTG      96
183 Asp Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val
184          1          5          10
186 TCC CCA GGA CAG ACG GCC GGG TTC ACC TGT GGG GGA GAC AAC GTT GGA      144
187 Ser Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly
188          15          20          25
190 AGG AAA AGT GTA CAG TGG TAC CAG CAG AAG CCA CCG CAG GCC CCT GTG      192
191 Arg Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val
192          30          35          40
194 CTG GTC ATC TAT GCT GAC AGC GAA CGG CCC TCA GGG ATC CCT GCG CGA      240
195 Leu Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg
196 45          50          55          60
198 TTC TCT GGC TCC AAC TCA GGG AAC ACC GCC ACC CTG ACC ATC AGC GGG      288
199 Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly
200          65          70          75
202 GTC GAG GCC GGG GAT GAG GCT GAC TAT TAC TGT CAG GTG TGG GAC AGT      336
203 Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser
204          80          85          90
206 ACT GCT GAT CAT TGG GTC TTC GGC GGA GGG ACC CGG CTG ACC GTC CTA      384
207 Thr Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu

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208          95          100          105
210 GGT
211 Gly
215 (2) INFORMATION FOR SEQ ID NO: 4:
217     (i) SEQUENCE CHARACTERISTICS:
218         (A) LENGTH: 128 amino acids
219         (B) TYPE: amino acid
220         (D) TOPOLOGY: linear
222     (ii) MOLECULE TYPE: protein
224     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
226 Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp
227 -19          -15          -10          -5
229 Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser
230          1          5          10
232 Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly Arg
233          15          20          25
235 Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val Leu
236 30          35          40          45
238 Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe
239          50          55          60
241 Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val
242          65          70          75
244 Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Thr
245          80          85          90
247 Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly
248 95          100          105
251 (2) INFORMATION FOR SEQ ID NO: 5:
253     (i) SEQUENCE CHARACTERISTICS:
254         (A) LENGTH: 702 base pairs
255         (B) TYPE: nucleic acid
256         (C) STRANDEDNESS: single
257         (D) TOPOLOGY: linear
259     (ii) MOLECULE TYPE: DNA (genomic)
261     (vi) ORIGINAL SOURCE:
262         (A) ORGANISM: Homo sapiens
264     (viii) POSITION IN GENOME:
265         (A) CHROMOSOME/SEGMENT: lambda variable and constant domains in
266                                CE9.1
268     (ix) FEATURE:
269         (A) NAME/KEY: CDS
270         (B) LOCATION: 1..702
272     (ix) FEATURE:
273         (A) NAME/KEY: mat_peptide
274         (B) LOCATION: 1..702
277     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
279 ATG GCC TGG GCT CTG CTG CTC CTC GGC CTC CTT GCT CAC TTT ACA GAC
280 Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp
281 1          5          10          15
283 TCT GCG GCC TCC TAT GAG TTG AGT CAG CCT CGC TCA GTG TCC GTG TCC
283          96

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284 Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser
285          20          25          30
287 CCA GGA CAG ACG GCC GGG TTC ACC TGT GGG GGA GAC AAC GTT GGA AGG      144
288 Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly Arg
289          35          40          45
291 AAA AGT GTA CAG TGG TAC CAG CAG AAG CCA CCG CAG GCC CCT GTG CTG      192
292 Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val Leu
293          50          55          60
295 GTC ATC TAT GCT GAC AGC GAA CGG CCC TCA GGG ATC CCT GCG CGA TTC      240
296 Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe
297 65          70          75          80
299 TCT GGC TCC AAC TCA GGG AAC ACC GCC ACC CTG ACC ATC AGC GGG GTC      288
300 Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val
301          85          90          95
303 GAG GCC GGG GAT GAG GCT GAC TAT TAC TGT CAG GTG TGG GAC AGT ACT      336
304 Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Thr
305          100          105          110
307 GCT GAT CAT TGG GTC TTC GGC GGA GGG ACC CGG CTG ACC GTC CTA GGT      384
308 Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly
309          115          120          125
311 CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT GAG      432
312 Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
313          130          135          140
315 GAG CTT CAA GCC AAC AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC TTC      480
316 Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
317 145          150          155          160
319 TAC CCG GGA GCC GTG ACA GTG GCC TGG AAG GCA GAT AGC AGC CCC GTC      528
320 Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
321          165          170          175
323 AAG GCG GGA GTG GAG ACC ACC ACA CCC TCC AAA CAA AGC AAC AAC AAG      576
324 Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
325          180          185          190
327 TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG TGG AAG TCC      624
328 Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
329          195          200          205
331 CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG GAG      672
332 His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
333          210          215          220
335 AAG ACA GTG GCC CCT ACA GAA TGT TCA TGA      702
336 Lys Thr Val Ala Pro Thr Glu Cys Ser
337 225          230
340 (2) INFORMATION FOR SEQ ID NO: 6:
342 (i) SEQUENCE CHARACTERISTICS:
343 (A) LENGTH: 233 amino acids
344 (B) TYPE: amino acid
345 (D) TOPOLOGY: linear
347 (ii) MOLECULE TYPE: protein
349 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
351 Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\09042001\I612914A.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]